



Information Hyperlinked  
over proteins

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Gene Model

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Symbol	Name	Synonyms	Organism
<b>PSMC2</b>	proteasome (prosome, macropain) 26S subunit, ATPase, 2	26S protease regulatory subunit 7, 26S proteasome AAA-ATPase subunit RPT1, MGC3004, MSS1, Nb1a10058, Proteasome 26S subunit ATPase 2, Protein MSS1, S7	Homo sapiens

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UniProt

P35968,

Q9LIA5,

Q9UD13

IntAct

P35993

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OMIM

154385

NCBI Gene

5701

NCBI RefSeq

NP\_002794

NCBI RefSeq

NM\_002893

NCBI UniGene

5701

NCBI Accession

BAE45763,

EAL24412

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HEC is not a part of the 26 S proteasome and interacts with MSS1 only when it is dissociated from the complex during M phase. [1997]

S2 bound to two ATPases, S4 and S7 . [2000]

S2 formed an immunoprecipitable heterotrimer upon co-translation with S4 and S7 . [2000]

The non-ATPase S5b also formed a ternary complex with [S4](#) and [S7](#) and the three proteins assembled into a tetramer with [S2](#). [2000]

The use of chimeric ATPases demonstrated that [S2](#) binds the NH(2)-terminal region of [S4](#) and the COOH-terminal two-thirds of [S7](#). [2000]

Mapping subunit contacts in the regulatory complex of the 26 S proteasome. [S2](#) and S5b form a tetramer with ATPase subunits [S4](#) and [S7](#). [2000]

Our results suggest that [MSS1](#) has a key role in activation of [HIV](#) genes regulated by Tat. [1992]

Furthermore, we provide evidence that expression of [MSS1](#) enhances the Tat-mediated [transactivation](#). [1992]

The [MSS1](#) protein shares 42% sequence identity with the human TBP-1 protein, which binds Tat *in vitro* and suppresses Tat-mediated [transactivation](#) in vivo (ref. 6). We report here that the levels of [HIV](#) activation by Tat correlate with endogenous levels of [MSS1](#) messenger RNA. [1992]

Peptide sequencing identifies [MSS1](#), a modulator of [HIV](#) Tat-mediated [transactivation](#), as subunit 7 of the 26 S protease. [1993]

[Peptide sequence analysis](#) reveals that 22 amino acids from the N-terminus of subunit 7 correspond exactly to the N-terminus of [MSS1](#), a modulator of [HIV](#) gene expression. [1993]

These results show that [HEC](#) is a negative regulator of [MSS1](#) and suggest that it may modulate [M phase](#) progression, in part, through the regulation of proteasome-mediated degradation of [cell cycle](#) regulatory proteins. [1997]

Here the [nucleotide sequence](#) of a [Xenopus](#) homologue of the human [MSS1](#) gene, a positive modulator of the [HIV-1](#) Tat mediated [transactivation](#) in mammalian cells, is presented. [1995]

Additional internal peptides from subunit 7 obtained by CNBr cleavage also match 100% with the deduced [amino acid sequence](#) of [MSS1](#). [1993]

Based on the fact that directly sequenced peptides from subunit 7 are identical to more than 12% of the hypothetical translation product of [MSS1](#), and the fact that the [molecular weight](#) of subunit 7 (49 kDa) corresponds to the predicted [molecular weight](#) of [MSS1](#) (48,633 Da), we conclude that subunit 7 is [MSS1](#). [1993]

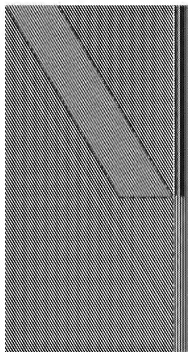
[Glycerol](#) gradient sedimentation analysis revealed that [MSS1](#) is included in protein complexes whose density is lighter than that of the proteasome. [2000]

However, the ratio of [MSS1](#) to 20S varied greatly among tissues and [MSS1](#) was concentrated in the [thymus](#). [2000]

A homologue of the human [MSS1](#) gene, a positive modulator of [HIV-1 gene expression](#), is massively expressed in [Xenopus coxys](#). [1995]

To recover the relationships among cichlasomine genera and to test their monophyly we analyzed sequences from two mitochondrial (16S rRNA, [cytochrome b](#)) and one nuclear marker (first [intron](#) of [S7](#) ribosomal gene) totalling 2236bp. [2008]

We present [DNA sequence](#) data from the mitochondrial [cytochrome b](#) ([cytb](#)) gene, the nuclear encoded [S7](#) [intron 1](#), and discretely coded external morphological characters for all 20 species in the darter clade Nothodontus. [2008]



The phylogenies resulting from analysis of the morphological dataset lack resolution, but nodes present are found in the cytb and S7 171 gene trees. [2008]



MSSP gene-2 encodes at least three alternative splicing products, MSSP-1 171, MSSP-2, and Scr2, which have been implied to function as factors regulating DNA replication, transcription, apoptosis induction, and cell-cycle movement, via the interaction with C-MYC. [1998]



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Special thanks to Chris Sander for his continuing support.